

What is claimed is:

1. A method for controlling starch synthesis in tomatoes comprising:
providing a population of plants derived from interspecific crosses of
5 *Lycopersicon* spp. with *Lycopersicon esculentum* genotypes; and
selecting individuals of said population that each contain an allele of a gene that
increases starch synthesis, said gene originating from said *Lycopersicon* spp.
2. The method according to claim 1 wherein said step of selecting comprises
selecting individuals that each contain the allele of the gene that encodes for an enzyme that
10 catalyzes a metabolic step in starch synthesis.
3. The method according to claim 1 wherein said step of selecting comprises
selecting individuals that each contain the allele of the gene that encodes for a subunit of
ADPGPPase.
4. The method according to claim 1 wherein said step of selecting comprises
15 selecting individuals that each contain the allele of the gene that encodes for a *Lycopersicon*
hirsutum-derived subunit of ADPGPPase.
5. The method according to claim 1 wherein said step of selecting comprises
selecting by using a molecular marker for said gene.
6. The method according to claim 5 wherein said molecular marker comprises step
20 of selecting comprises a *Lycopersicon hirsutum*-derived large subunit (LS1) of ADPGPPase.
7. The method according to claim 2 wherein said step of selecting comprises
selecting by measuring activity of said enzyme in young fruit and selecting those young fruit
with high activity of said enzyme.
8. The method according to claim 2 wherein said step of selecting comprises
25 selecting by measuring ADPGPPase activity of said young fruit, and selecting those young fruit
with high ADPGPPase activity.
9. The method according to claim 1 wherein said *Lycopersicon* spp. comprises a
Lycopersicon spp. of green-fruited *Eriopersicon* subgenus.
10. The method according to claim 1 wherein said *Lycopersicon* spp. comprises
30 *Lycopersicon hirsutum*.
11. A method of producing genetically transformed plants which have elevated starch
content, comprising the steps of:
a) inserting into the genome of a plant cell a recombinant double stranded DNA

molecule comprising

(i) a selected promoter

(ii) a structural DNA sequence that causes the production of an RNA sequence which encodes the above described ADPGPPase LS1 protein

5 b) obtaining transformed plant cells

c) regenerating from the transformed plant cells genetically transformed plants with elevated starch content.

10 12. The method according to claim 11 wherein said plant cell is selected from the group consisting of a tomato cell, a potato cell, a cell from a solanaceous plant, a legume cell, and a grain crop cell.

13. The method according to claim 11 wherein said promoter is selected from the group consisting of an immature fruit promoter, a tuber promoter, and a seed promoter.

14. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in an immature fruit.

15 15. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in a tuber.

16. The method according to claim 11 wherein said step of regenerating comprises regenerating genetically transformed plants with elevated starch content in a seed.

20 17. A method according to claim 1 and additionally comprising the step of propagating said individuals of said population.

18. A method according to claim 17 wherein the step of propagating includes the step of vegetative propagation.

19. A method according to claim 17 wherein the step of propagating includes the step of propagation by seed.

25 20. A method according to claim 11 and additionally comprising the step of propagating said genetically transformed plants.

21. A method according to claim 20 wherein the step of propagating includes the step of vegetative propagation.

30 22. A method according to claim 20 wherein the step of propagating includes the step of propagation by seed.

23. A plant produced according to the method of claim 1.

24. A plant produced according to the method of claim 11.

25. A fruit produced by a plant in accordance with claim 23.

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b)

26. A fruit produced by a plant in accordance with claim 24.
27. A seed which when grown yields a plant in accordance with claim 23.
28. A seed which when grown yields a plant in accordance with claim 24.
29. A gene that controls sucrose-starch metabolism comprising a nucleotide sequence as

follows:

1 ATGAAATCGA CGGTTTCATTT GGGGAGAGTG AGCACTGGTG CTTTAACAA
51 TGGAGAGAAG GAGATTTTTG GGGAGAAGAT GAGAGGGAGT TTGAACAACA
101 ATCTCAGGAT TAATCAGTTG TCGAAAAGTT TGAAACTTGA GAAGAAGGAG
151 AAGAAGATTA AACCTGGGGT TGCTTACTCT GTGATCACTA CTGAAAATGA
201 CACAGAGACT GTGTTCTAG ATATGCCACG TCTTGAGAGA CGCCGGGCAA
251 ATCCCAAGGA TGTGGCTGCA GTCATATTAG GAGGAGGCGA AGGGACCAAG
301 TTATTCCAC TTACAAGTAG AACTGCAACC CCTGCTGTTT CGGTTGGAGG
351 ATGCTACAGG CTCATAGACA TCCCGATGAG CAACTGTATC AACAGTGCTA
401 TTAACAAGAT TTTTGTGCTG ACACAGTACA ATTCTGCTGC CCTGAATCGT
451 CACATTGCTC GAACGTATTT TGGCAATGGT GTGAGCTTTG GAGATGGATT
501 TGTCGAGGTA CTAGCTGCAA CTCAGACACC TGGGGAAGCA GGAAAAAAT
551 GGTTC AAGG AACAGCAGAT GCTGTCAGAA AATTTATATG GGTTCCTGAG
601 GACGCTAAGA ACAAGAATAT TGAAAATATC CTTGTATTAT CTGGGGATCA
651 TCTTTATAGG ATGCTATTATA TGGAGTTGGT GCAGAACCAT ATTGACAGAA
701 ATGCTGATAT TACTCTTTCA TGTGCACCAG CTGAGGACAG CCGAGCATCA
751 GATTTTGGGC TGGTCAAGAT TGACAGCAGA GGCAGAGTTG TCCAGTTTGC
801 TGAAAAACCA AAAGGTTTGT AGCTTAAAGC AATGCAAGTA GATACTACTC
851 TTGTTGGATT ATCTCCAGAA GATGCGAAGA AATCCCCTTA TATTGCTTCA
901 ATGGGAGTTT ATGTTTTCAG GACAGATGTA TTGCTGAAGC TCTTGAAATG
951 GAGCTACCCC ACTTCTAATC ATTTTGGCTC TGAAATTATA CCAGCAGCTA
1001 TTGATGATTA CAATGTCCAA GCATACATTT TCAAAGACTA TTGGGAGGAC
1051 ATTGGAACAA TTAAATCTTT CTATAATGCT AGCTTGGCGC TCACACAAGA
1101 GTTTCAGAG TTCCAATTTT ATGATCCAAA AACACCTTTT TACACATCTC
1151 CTAGGTTTCT TCCACCAACC AAGATAGACA ATTGCAAGAT TAAGGATGCC
1201 ATAATTTCTC ATGGATGTTT CTTGCGAGAT TGCTCTGTGG AACACTCCAT
1251 AGTGGGTGAA AGATCACGCT TAGACTGTGG TGTGAACTG AAGGATACTT
1301 TCATGATGGG AGCAGACTAC TACCAACAG AATCTGAGAT TGCCTCCCTG
1351 TTAGCAGAGG GGAAAGTACC GATTGGGATT GGGGAAAATA CAAAAATAAG
1401 GAAATGTATC ATTGACAAGA ACGCAAAGAT AGGAAAAAAT GTTTCAATCA
1451 TTAATAAAGA TGGTGTTCAG GAGGCAGACC GACCAGAGGA AGGATTCTAC
1501 ATACGATCAG GGATAACCAT TATATCAGAG AAAGCCACAA TTAGAGATGG
1551 AACAGTTATA TGA

30. A protein that controls sucrose-starch metabolism comprising a derived amino acid sequence as follows:

MKSTVHLGRVSTGGFNNGEKEIFGEKMRGSLNNNLRINQL
SKSLKLEKKEKKIKPGVAYSVITTENDTETVFVDMRRLERRAN
PKDVAAVILGGGEGTKLFPLTSRTATPAVPVGGCYRLIDIPMSNC
INSAINKIFVLTQYNSAALNRHIARTYFGNGVSFGDGFVEVLAAT
QTPGEAGKKWFQGTADAVRKFIWVFEDAKNKNENILVLSGDHL
YRMDYMEVLVQNHIDRNADITLSCAPAEDSRASDFGLVKIDSRGR

VVQFAEKPKGFELKAMQVDTTLVGLSPQDAKKSPYIASMGVYV
FKTDVLLKLLKWSYPTSNDFGSEIIPAAIDYINVQAYIFKDYWED
IGTIKSFYNASLALTQEFFEFQFYDPKTPFYTSRFLPPTKIDNCKI
KDAISHGCFLRDCSVEHSIVGERSRLDCGVELKDTFMMGADYY
5 QTESEIASLLAEGKVPIGIGENTKIRKCIIDKNAKIGKNVSIINKDG
VQEADRPEEGFYIRSGITIISEKATIRDGTVI

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